



ENTERED

OIPF

RAW SEQUENCE LISTING

DATE: 03/04/2002

PATENT APPLICATION: US/10/076,260

TIME: 16:03:40

Input Set : A:\02076seq.txt

Output Set: N:\CRF3\03042002\J076260.raw

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3 <110> APPLICANT: Elliott, Steven G.
4     Rogers, Norma
5     Busse, Leigh Anne
7 <120> TITLE OF INVENTION: G-Protein Coupled Receptor Molecules and Uses Thereof
9 <130> FILE REFERENCE: 02-076
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/076,260
C--> 12 <141> CURRENT FILING DATE: 2002-02-14
14 <150> PRIOR APPLICATION NUMBER: 60/269,040
15 <151> PRIOR FILING DATE: 2001-02-14
17 <160> NUMBER OF SEQ ID NOS: 22
19 <170> SOFTWARE: PatentIn Ver. 2.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1038
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
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35 gtg atg ccg ccg ctg ctc att gtg gcc ttt gtg ctg ggc gca cta ggc      96
36 Val Met Pro Pro Leu Leu Ile Val Ala Phe Val Leu Gly Ala Leu Gly
37   20              25              30
39 aat ggg gtc gcc ctg tgt ggt ttc tgc ttc cac atg aag acc tgg aag      144
40 Asn Gly Val Ala Leu Cys Gly Phe Cys Phe His Met Lys Thr Trp Lys
41   35              40              45
43 ccc agc act gtt tac ctt ttc aat ttg gcc gtg gct gat ttc ctc ctt      192
44 Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu
45   50              55              60
47 atg atc tgc ctg cct ttt cgg aca gac tat tac ctc aga cgt aga cac      240
48 Met Ile Cys Leu Pro Phe Arg Thr Asp Tyr Tyr Leu Arg Arg Arg His
49   65              70              75              80
51 tgg gct ttt ggg gac att ccc tgc cga gtg ggg ctc ttc acg ttg gcc      288
52 Trp Ala Phe Gly Asp Ile Pro Cys Arg Val Gly Leu Phe Thr Leu Ala
53   85              90              95
55 atg aac agg gcc ggg agc atc gtg ttc ctt acg gtg gtg gct gcg gac      336
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57   100             105             110
59 agg tat ttc aaa gtg gtc cac ccc cac cac gcg gtg aac act atc tcc      384
60 Arg Tyr Phe Lys Val Val His Pro His His Ala Val Asn Thr Ile Ser
61   115             120             125

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63 acc cgg gtg gcg gct ggc atc gtc tgc acc ctg tgg gcc ctg gtc atc 432
64 Thr Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile
65 130 135 140
67 ctg gga aca gtg tat ctt ttg ctg gag aac cat ctc tgc gtg caa gag 480
68 Leu Gly Thr Val Tyr Leu Leu Leu Glu Asn His Leu Cys Val Gln Glu
69 145 150 155 160
71 acg gcc gtc tcc tgt gag agc ttc atc atg gag tcg gcc aat ggc tgg 528
72 Thr Ala Val Ser Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp
73 165 170 175
75 cat gac atc atg ttc cag ctg gag ttc ttt atg ccc ctc ggc atc atc 576
76 His Asp Ile Met Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile
77 180 185 190
79 tta ttt tgc tcc ttc aag att gtt tgg agc ctg agg cgg agg cag cag 624
80 Leu Phe Cys Ser Phe Lys Ile Val Trp Ser Leu Arg Arg Arg Gln Gln
81 195 200 205
83 ctg gcc aga cag gct cgg atg aag aag gcg acc cgg ttc atc atg gtg 672
84 Leu Ala Arg Gln Ala Arg Met Lys Lys Ala Thr Arg Phe Ile Met Val
85 210 215 220
87 gtg gca att gtg ttc atc aca tgc tac ctg ccc agc gtg tct gct aga 720
88 Val Ala Ile Val Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg
89 225 230 235 240
91 ctc tat ttc ctc tgg acg gtg ccc tcg agt gcc tgc gat ccc tct gtc 768
92 Leu Tyr Phe Leu Trp Thr Val Pro Ser Ser Ala Cys Asp Pro Ser Val
93 245 250 255
95 cat ggg gcc ctg cac ata acc ctc agc ttc acc tac atg aac agc atg 816
96 His Gly Ala Leu His Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met
97 260 265 270
99 ctg gat ccc ctg gtg tat tat ttt tca agc ccc tcc ttt ccc aaa ttc 864
100 Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Lys Phe
101 275 280 285
103 tac aac aag ctc aaa atc tgc agt ctg aaa ccc aag cag cca gga cac 912
104 Tyr Asn Lys Leu Lys Ile Cys Ser Leu Lys Pro Lys Gln Pro Gly His
105 290 295 300
107 tca aaa aca caa agg ccg gaa gag atg cca att tcg aac ctc ggt cgc 960
108 Ser Lys Thr Gln Arg Pro Glu Glu Met Pro Ile Ser Asn Leu Gly Arg
109 305 310 315 320
111 agg agt tgc atc agt gtg gca aat agt ttc caa agc cag tct gat ggg 1008
112 Arg Ser Cys Ile Ser Val Ala Asn Ser Phe Gln Ser Gln Ser Asp Gly
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133          35          40          45
135 Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu
136          50          55          60
138 Met Ile Cys Leu Pro Phe Arg Thr Asp Tyr Tyr Leu Arg Arg Arg His
139          65          70          75          80
141 Trp Ala Phe Gly Asp Ile Pro Cys Arg Val Gly Leu Phe Thr Leu Ala
142          85          90          95
144 Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Asp
145          100         105         110
147 Arg Tyr Phe Lys Val Val His Pro His His Ala Val Asn Thr Ile Ser
148          115         120         125
150 Thr Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile
151          130         135         140
153 Leu Gly Thr Val Tyr Leu Leu Leu Glu Asn His Leu Cys Val Gln Glu
154          145         150         155         160
156 Thr Ala Val Ser Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp
157          165         170         175
159 His Asp Ile Met Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile
160          180         185         190
162 Leu Phe Cys Ser Phe Lys Ile Val Trp Ser Leu Arg Arg Arg Gln Gln
163          195         200         205
165 Leu Ala Arg Gln Ala Arg Met Lys Lys Ala Thr Arg Phe Ile Met Val
166          210         215         220
168 Val Ala Ile Val Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg
169          225         230         235         240
171 Leu Tyr Phe Leu Trp Thr Val Pro Ser Ser Ala Cys Asp Pro Ser Val
172          245         250         255
174 His Gly Ala Leu His Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met
175          260         265         270
177 Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Lys Phe
178          275         280         285
180 Tyr Asn Lys Leu Lys Ile Cys Ser Leu Lys Pro Lys Gln Pro Gly His
181          290         295         300
183 Ser Lys Thr Gln Arg Pro Glu Glu Met Pro Ile Ser Asn Leu Gly Arg
184          305         310         315         320
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196 <213> ORGANISM: Mus musculus
198 <220> FEATURE:
199 <221> NAME/KEY: CDS
200 <222> LOCATION: (350)..(1402)

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207 cgcttgacc ccagagcctg acccagctgc aggcctcaac tctgtagggg acgtgcagct 180
209 cgtgatccaa gcctaggaga aaggacttgc tgccggcttt catttcctgg ctgaagtttc 240
211 tctcgtgggt gcagcgctg catcccaggg tgatgagggt aggggcccag ctgctagagg 300
213 agccctagtg ttcggatagg cagctgtgcc tctgtgccgg ccaccttgg atg cca gtc 358
214                                     Met Pro Val
215                                     1
217 ctc tct cca act gct atg gac aac ggg tcg tgc tgt ctc atc gag ggg 406
218 Leu Ser Pro Thr Ala Met Asp Asn Gly Ser Cys Cys Leu Ile Glu Gly
219      5          10          15
221 gag ccc atc tcc cag gtg atg cct cct cta ctc atc ctg gtc ttc gtg 454
222 Glu Pro Ile Ser Gln Val Met Pro Pro Leu Leu Ile Leu Val Phe Val
223 20          25          30          35
225 ctt ggc gcc ctg ggc aac ggc ata gcc ctg tgc ggc ttc tgc ttt cac 502
226 Leu Gly Ala Leu Gly Asn Gly Ile Ala Leu Cys Gly Phe Cys Phe His
227      40          45          50
229 atg aag acc tgg aag tca agc act att tac ctt ttc aac ttg gct gtg 550
230 Met Lys Thr Trp Lys Ser Ser Thr Ile Tyr Leu Phe Asn Leu Ala Val
231      55          60          65
233 gcc gat ttt ctc ctc atg atc tgc tta ccc ctt cgg aca gac tac tac 598
234 Ala Asp Phe Leu Leu Met Ile Cys Leu Pro Leu Arg Thr Asp Tyr Tyr
235      70          75          80
237 ctc aga cgc aga cac tgg att ttt gga gat atc gcc tgt cgc ctg gtc 646
238 Leu Arg Arg Arg His Trp Ile Phe Gly Asp Ile Ala Cys Arg Leu Val
239      85          90          95
241 ctc ttc aag ctg gcc atg aat agg gcc ggg agc att gtc ttc ctc act 694
242 Leu Phe Lys Leu Ala Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr
243 100          105          110          115
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247      120          125          130
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250 Val Asn Ala Ile Ser Asn Arg Thr Ala Ala Ala Thr Ala Cys Val Leu
251      135          140          145
253 tgg act ttg gtc atc ttg ggg act gtg tat ctt ctg atg gag agt cac 838
254 Trp Thr Leu Val Ile Leu Gly Thr Val Tyr Leu Leu Met Glu Ser His
255      150          155          160
257 ctg tgt gtg cag ggg aca ctg tcg tcc tgt gag agc ttc atc atg gag 886
258 Leu Cys Val Gln Gly Thr Leu Ser Ser Cys Glu Ser Phe Ile Met Glu
259      165          170          175
261 tca gcc aac ggg tgg cac gat gtc atg ttc cag ctg gag ttc ttc ctg 934
262 Ser Ala Asn Gly Trp His Asp Val Met Phe Gln Leu Glu Phe Phe Leu
263 180          185          190          195
265 ccc ctg aca atc atc ttg ttc tgc tcg gtc aac gtt gtt tgg agc ctg 982
266 Pro Leu Thr Ile Ile Leu Phe Cys Ser Val Asn Val Val Trp Ser Leu
267      200          205          210
269 aga cgg agg cag cag ctg acc aga cag gct cgg atg agg agg gcc acc 1030

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270 Arg Arg Arg Gln Gln Leu Thr Arg Gln Ala Arg Met Arg Arg Ala Thr
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273 cgg ttc atc atg gtg gtg gct tct gtg ttc atc acg tgt tac ctg ccc 1078
274 Arg Phe Ile Met Val Val Ala Ser Val Phe Ile Thr Cys Tyr Leu Pro
275          230          235          240
277 agc gtg ctg gct agg ctc tac ttc ctc tgg acg gtg ccc act agt gcc 1126
278 Ser Val Leu Ala Arg Leu Tyr Phe Leu Trp Thr Val Pro Thr Ser Ala
279          245          250          255
281 tgt gac ccc tct gtc cac aca gcc ctc cac gtc acc ctg agc ttc acc 1174
282 Cys Asp Pro Ser Val His Thr Ala Leu His Val Thr Leu Ser Phe Thr
283 260          265          270          275
285 tac ctg aac agt atg ctg gat ccc ctt gta tat tac ttc tca agc ccc 1222
286 Tyr Leu Asn Ser Met Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ser Pro
287          280          285          290
289 tcg ctc ccc aaa ttc tac gcc aag ctc aca atc tgc agc ctg aag ccc 1270
290 Ser Leu Pro Lys Phe Tyr Ala Lys Leu Thr Ile Cys Ser Leu Lys Pro
291          295          300          305
293 aaa cgc cca gga cgc acg aag acg cgg agg tca gaa gag atg cca att 1318
294 Lys Arg Pro Gly Arg Thr Lys Thr Arg Arg Ser Glu Glu Met Pro Ile
295          310          315          320
297 tcg aac ctc tgc agt aag agc tcc atc gat ggg gca aat cgt tcc cag 1366
298 Ser Asn Leu Cys Ser Lys Ser Ser Ile Asp Gly Ala Asn Arg Ser Gln
299          325          330          335
301 agg cca tct gac ggg cag tgg gat ctc caa gtg tgt tgaatgccat 1412
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345 ctttcaagcc acaaaagtgg tgacagccat tcaactctct cagttcccag ggtactctcc 2672
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L:11 M:270 C: Current Application Number differs, Replaced Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date